STIC-Biotech/ChemLib 74587

From: Fredman, Jeffrey
Sent: Tuesday, August 06, 2002 12:12 PM
To: STIC-Biotech/ChemLib
Cc: Chunduru, Suryaprahbha
Subject: FW: ref to rush seq search fo SN# 09/786,105

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----
From: Chunduru, Suryaprahbha
Sent: Tuesday, August 06, 2002 11:49 AM
To: Fredman, Jeffrey
Subject: ref to rush seq search fo SN# 09/786,105

Hi Jeff,
I need a rush sequence search on the following. I need your approval on this rush sequence search since the case is due for this biweek.

1. Application Serial NO. 09/786,105, SEQ ID Nos. 1-4 (primers)
(Search is requested for all commercial nucleic acid, oligomer and issued patent databases).

Thank you
Suryaprabha Chunduru
Examiner
Art Unit 1637
Room No. 10D06
Mail Room No. 10E12.
Tel. No. 305-1004.

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 8/7
Date Completed: 8/8
Searcher Prep/Review: 1/2
Clerical: _____
Online time: 1/2

TYPE OF SEARCH:
NA Sequences: 8
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 0
WWW/Internet: _____
Other (specify): _____

L Number	Hits	Search Text	DB	Time stamp
1	8878	primer adj1 design or select$ adj1 program	USPAT; US-PGPUB; DERWENT	2002/08/12 09:32
2	0	(primer adj1 design or select$ adj1 program) near5 mycobacteria	USPAT; US-PGPUB; DERWENT	2002/08/12 09:32
3	19	(primer adj1 design or select$ adj1 program) and mycobacteria	USPAT; US-PGPUB; DERWENT	2002/08/12 09:33

1: Nucleic Acids Res 1990 Apr 11;18(7):1757-61 Related Articles, Books, LinkOut

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Related Resources

A computer program for selection of oligonucleotide primers for polymerase chain reactions.

Lowe T, Sharefkin J, Yang SQ, Dieffenbach CW.

Department of Surgery, Uniformed Services University of the Health Sciences, Bethesda, MD 20814.

We have designed a computer program which rapidly scans nucleic acid sequences to select all possible pairs of oligonucleotides suitable for use as primers to direct efficient DNA amplification by the polymerase chain reaction. This program is based on a set of rules which define in generic terms both the sequence composition of the primers and the amplified region of DNA. These rules (1) enhance primer-to-target sequence hybridization avidity at critical 3'-end extension initiation sites, (2) facilitate attainment of full length extension during the 72 degrees C phase, by minimizing generation of incomplete or nonspecific product and (3) limit primer losses occurring from primer-self or primer-primer homologies. Three examples of primer sets chosen by the program that correctly amplified the target regions starting from RNA are shown. This program should facilitate the rapid selection of effective and specific primers from long gene sequences while providing a flexible choice of various primers to focus study on particular regions of interest.

PMID: 1692404 [PubMed - indexed for MEDLINE]

1: J Virol Methods 1992 Feb;36(2):119-28

OLIGSCAN: a computer program to assist in the design of PCR primers homologous to multiple DNA sequences.

Montpetit ML, Cassol S, Salas T, O'Shaughnessy MV.

Federal Centre for AIDS, Health and Welfare Canada, Ottawa, Ontario.

OLIGSCAN (oligonucleotide scanner) is a computer program for IBM-PC-compatible computers that allows the user to scan up to 200 DNA sequences for homology to oligonucleotide sequences of interest. Once a core sequence of longer than the user-defined minimum length is found, the remainder of the oligonucleotide is compared to the corresponding positions of the larger sequence to identify matches or mismatches flanking the core region. This algorithm results in identification of the longest possible homologous regions first. The program was originally designed to assist in the identification of potential annealing sites for polymerase chain reaction (PCR) primers in the genomic DNA of related strains of viruses. However, it may also be used for more general pattern-identification purposes, including scanning for various sequence motifs of functional importance. We present the analysis of homology to an oligonucleotide primer in 16 complete genomic sequences of the human and simian immunodeficiency viruses.

PMID: 1556160 [PubMed - indexed for MEDLINE]

1: J Virol Methods 1993 Feb;41(2):157-65 Related Articles, Books, LinkOut

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Related Resources

A computer program for the design of PCR primers for diagnosis of highly variable genomes.

Dopazo J, Sobrino F.

INIA-Sanidad Animal, Madrid, Spain.

PCRDiag (Diagnosis by PCR) is a computer program which allows the localization of pairs of oligonucleotides with optimal thermodynamic requirements for use in a PCR assay. The program is designed for the selection of pairs of primers complementary to sequences present in a group, whose identification is intended, but are absent in other non-specific sequences. The program constitutes a powerful tool, specially in systems which display a high degree of sequence heterogeneity, as is the case of RNA viruses. The program runs on IBM-PC and compatible computers and has no special software requirements. It does not need the previous alignment of the sequences analyzed.

PMID: 8388397 [PubMed - indexed for MEDLINE]

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L13 ANSWER 13 OF 14 CAPLUS COPYRIGHT 2002 ACS
AN 1992:167274 CAPLUS
DN 116:167274
TI OSP: a computer program for choosing PCR and DNA sequencing primers
AU Hillier, LaDeana; Green, Philip
CS Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SO PCR Methods Appl. (1991), 1(2), 124-8
CODEN: PMAPES; ISSN: 1054-9803
DT Journal
LA English
AB OSP (Oligonucleotide Selection Program) selects oligonucleotide primers for DNA sequencing and the polymerase chain reaction (PCR). The user can specify (or use default) constraints for primer and amplified product lengths, %(G+C), (abs. or relative) melting temps., and primer 3' nucleotides. To help minimize nonspecific priming and primer secondary structure, OSP screens candidate primer sequences, using user-specifiable cutoffs, against potential base-pairing with a variety of sequences present in the reaction, including the primer itself, the other primer (for PCR), the amplified product, and any other sequences desired (e.g., repetitive element sequences in genomic templates, vector sequence in cloned templates, or other primer pair sequences in multiplexed PCR reactions). Base-pairing involving the primer 3' end is considered sep. from base-pairing involving internal sequences. Primers meeting all constraints are ranked by a combined score, a user definable weighted sum of any of the above parameters. OSP is being routinely and extensively used to select sequencing primers for the Caenorhabditis elegans genome sequencing project and human genomic PCR primer pairs for the Washington University Genome Center mapping project, with success rates exceeding 96% and 81%, resp. It is available for research purposes from the authors, at no cost, in both text output and interactive graphics (X windows) versions.

L13 ANSWER 11 OF 14 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 4

AN 1994:251395 BIOSIS

DN PREV199497264395

TI A **computer**-aided **selection** of oligonucleotide **primer** for polymerase chain reaction.

AU Li, Chibo; Wu, Chungen; Zheng, Baofen

CS Dep. Biophysics, Sch. Basic Med. Sci., Shanghai Med. Univ., Shanghai China

SO Acta Academiae Medicinae Shanghai, (1994) Vol. 21, No. 2, pp. 143-145. ISSN: 0257-8131.

DT Article

LA Chinese

SL Chinese; English

AB We have designed a computer program which can scan nucleic acid sequences to select primers for polymerase chain reaction. This program is based on a set of rules for selection primers. These rules include: (1) Primers should contain a GC-type sequence pair at their 3' end; (2) The length of each primer should be between 18 to 24 nucleotides; (3) Each primer should have a GC-type sequence content of between 45% to 60% of its total bases; (4) Limit primer loss occurring from primer-self or primer-primer homologies. We have designed a pair of primers of SRS leukemia virus by this method, and successfully amplified 3.4 kb products of interest. The results satisfied the effectiveness and specificity of primers selected by this method.